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1 GTCCTTCCACCATGCACTCGCTGGGCTTCTTCTGTGGCGTGTCTCTCTGCTCGCCCGCTG 60
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
CAGGAAGGTGCTACGTAGCGACCCGAGAGAGACACCGCACACAGAGACGAGCGCGGAC
M H S L G F F S V A C S L L A A A -
CGCTGCTCCCGGTCCTCGGAGGCGCCCGCCCGCCCGCCCTTCGAGTCCGGACTCG 120
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
GCGACGAGGCCCCAGGAGCGCTCCGCGGGCGGGCGGGGGAAGCTCAGGCCCTGAGC
L L P G P R E A P A A A A F E S G L D -
ACCTCTCGGACGGAGCCCCGACGGCGGGCGAGGCCACGGCTTATGCAAGCAAAGATCTGG 180
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
TGGAGAGCCTGCGCCCTCGGGCTGCGGCCCGCTCCGGTGCCGAATACGTTCTGTCTAGACC
L S D A E P D A G E A T A Y A S K D L E -
AGGAGCAGTTACGGTCTGTGTCCAGGTAGATGAACCTCATGACTGTACTCTACCCAGAAT 240
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
TCCTCGTCAATGCCAGACACAGGTCACATCTACTTGAGTACTGACATGAGATGGGTCTTA
E Q L R S V S S V D E L M T V L Y P E Y -
ATTGGAAAAATGTACAAGTGTCAAGCTAAGGAAAGGAGGCTGGCAACATAACAGAGAACAGG 300
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
TAACCTTTTACATGTTACAGTCGATTCCTTTCCCTCCGACCGTTGTATTGTCTCTGTCC
W K M Y K C Q L R K G G W Q H N R E Q A -
CAAACCTCAACTCAAGGACAGAGACTATAAAATTGCTGCAGCACATTATAATACAG

MATCH WITH FIG. 1B

FIG. 1A

MATCH WITH FIG. 1A

301 -----+-----+-----+-----+-----+-----+ 360
GGTTGGAGTTGAGTTCCTGCTCTCTGATATTTAACGACGTCGTTAATATATGTC
N L N S R T E E T I K F A A A H Y N T E -

AGATCTTGAAAAGTATTGATAATGAGTGGAGAAAGACTCAATGCATGCCACGGGAGGTGT
 361 -----+-----+-----+-----+-----+-----+-----+ 420

TCTAGAACTTTTCATACTATTACTCACCCTCTTTCTGAGTTACGTACGGTGCCCTCCACA
I L K S I D N E W R K T Q C M P R E V C -

GTATAGATGTGGGAAGGAGTTTGGAGTCGGGACAAACACCTTCTTTAAACCTCCATGTG
421 -----+-----+-----+-----+-----+-----+-----+ 480

CATATCTACACCCCTTCCTCAAACCTCAGCGCTGTTGTGGAAGAAATTGGAGGTACAC
I D V G K E F G V A T N T F F K P P C V -

181 TGTCCGCTACAGATGTGGGGTGTGCTGCAATAGTGAGGGGCTGCAGTGCATGAACACCA 540

ACAGGCAGATGTCTACACCCCCAACGACGTTATCACTCCCGACGTCACGTA CT TGTGGT
S V Y R C G G C C N S E G L O C M N T S -

GCACGAGCTACCTCAGCAAGACGTTATTTGAAATTACAGTGCCCTCTCTCAAGGCCCA
 41 -----+-----+-----+-----+-----+-----+-----+ 600

CGTGCTCGATGGAGTCGTTCTGCAATAAACTTTAATGTCAAGAGAGAGAGTTCGGGGT
T S Y L S K T L F E I T V P L S O G P K -

AACCAGTAACAATCAGTTTGGCCAATCACACTTCTGCCGATGCATGCTCTAAACTGGATG
01 -----+-----+-----+-----+-----+-----+-----+ 660

TTGGTCATTGTTAGTCAAAACGGTTAGTGTGAAGGACGGCTACGTACAGATTGACCTAC
P V T I S F A N H T S C R C M S K L D V -

MATCH WITH FIG. 1C

FIG. 1B

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V C K N K L F P S Q C G A N R E F D E N -

TGTGTACGGTCACACATACATTTCTTGGACGGGCTTTAGTTGGGATTAGGACCTT
T C C Q C C V C C K R T C P R N Q P L N P G K

TTACACGGACACTTACATGTCTTTCAGGTGCTTTACGAACAATTTCTCTTCACAGG
C A C E C T E S P Q K C L L K G K K F H

H Q T C S C Y R R P C T N R Q K A C E P
TGGTGGTTGTACGTCGACAAATGTCTGCCGGTACATGCTTGGCGGTCTTCCGAACACTCG

GTCCCTAAAGTATATCACTTCTCACACAGCAACACAGGAGTATAACCGTTTCTCTGGTG
G F S Y S E E V C R C V P S Y W O R P O

AAATGAGCTAAGATTGTACTGTGTTTCCAGTTCATCGATTTTCTATTATGGGAAACTGTGT

MATCH WITH FIG. 1E

MATCH WITH FIG. 1E

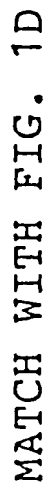


FIG. 1E

1 CGAGGCCACGGCTTATGCAAGCAAGATCTGGAGGAGCAGTTACGGTCTGTGTCCAGTGT
-----+-----+-----+-----+-----+-----+-----+
71 AGATGAACTCATGACTGTACTCTACCCAGAATATTGGAAATGTACAAGTGTCAAGCTAAG
-----+-----+-----+-----+-----+-----+-----+
M T V L Y P E Y W K M Y K C Q L R
-----+-----+-----+-----+-----+-----+-----+
121 GAAAGGAGGCTGGCAACATAACAGAGAACAGGCCAACCTCAACTCAAGGACAGAAGAGAC
-----+-----+-----+-----+-----+-----+-----+
K G G W Q H N R E Q A N L N S R T E E T
-----+-----+-----+-----+-----+-----+-----+
181 TATAAAATTTGCTGCAGCACATTATAATACAGAGATCTTGAAAGTATTGATAATGAGTG
-----+-----+-----+-----+-----+-----+-----+
I K F A A A H Y N T E I L K S I D N E W
-----+-----+-----+-----+-----+-----+-----+
241 GAGAAAGACTCAATGCATGCCACGGGAGGTGTGTATAGATGTGGGGAAGGAGTTTGGAGT
-----+-----+-----+-----+-----+-----+-----+
R K T Q C M P R E V C I D V G K E F G V
-----+-----+-----+-----+-----+-----+-----+
301 CGCGACAAACACCTTCTTTAAACCTCCATGTGTGTCCTCGTCTACAGATGTGGGGTGTGCTG
-----+-----+-----+-----+-----+-----+-----+
A T N T F F K P P C V S V Y R C G G C C

FIG. 2A

361 CAATAGTGGGGCTGCAGTGCATGAACACCAGCAGCTACCTCAGCAAGACGTTATT
N S E G L Q C M N T S T S Y L S K T L F
421 TGAAATTACAGTGCCTCTCTCTCAAGGCCCAACACAGTAACAATCAGTTTGGCCAATCA
E I T V P L S Q G P K P V T I S F A N H
481 CACTTCCTGCCGATGCATGTCTAAACTGGATGTTTACAGACAAGTTTCATTCCATTATTAG
T S C R C M S K L D V Y R Q V H S I I R
541 ACGTTCCCTGCCAGCAACTACCACAGTGTGAGCAGCGAACAAGACCTGCCCCACCAA
R S L P A T L P Q C Q A A N K T C P T N
601 TTACATGTGGAATAATCACATCTGCAGATGCCCTGGCTCAGGAAGATTTTATGTTTTCCTC
Y M W N N H I C R C L A Q E D F M F S S
661 GGATGCTGGAGATGACTCAACAGATGGATTCCATGACATCTGTGGACCAACAAGGAGCT
D A G D D S T D G F H D I C G P N K E L

FIG. 2B

721 GGATGAAGACCTGTCAAGTGTCTGCAGAGCGGGCTTCGGCCTGCCAGCTGTGGACC
D E E T C Q C V C R A G L R P A S C G P
781 CCACAAAGAACTAGACAGAACTCATGCCAGTGTGTCTGTAAACAACTCTTCCCCAG
H K E L D R N S C Q C V C K N K L F P S
841 CCAATGTGGGCCAACCGAGAATTGTGATGAACACATGCCAGTGTGTATGTAAGAAGAAC
Q C G A N R E F D E N T C Q C V C K R T
901 CTGCCCCAGAAATCAACCCCTAAATCCTCGGAAATGTGCCCTGTGAATGTACAGAAAGTCC
C P R N Q P L N P G K C A C E C T E S P
961 ACAGAAATGCTGTAAAGGAAGAAGTTCCACCACCAACATGCAGCTGTACAGACG
Q K C L L K G K K F H H Q T C S C Y R R
1021 GCCATGTACGAACCGCAGAGGCTTGTGAGCCAGGATTTTCATATAGTGAAGAAGTGTG
P C T N R Q K A C E P G F S Y S E E V C

FIG. 2C

1081 TCGTTGTGCCCTTCATATTGGCAAGACCACAAATGAGCTAAGATTGTTACTGTTTCCCA
-----+-----+-----+-----+-----+
R C V P S Y W Q R P Q M S
1141 GTTCATCGATTTTCTATTATGGAAACTGTGTGGCCACAGTAGAACTGTCTGTGAACAGA
-----+-----+-----+-----+-----+
1201 GAGACCCTGTGGGTCCCATGCTAACAAAGACAAAGTCTGTCTTTCCCTGAACCATGTGGA
-----+-----+-----+-----+-----+
1261 TAACTTTACAGAAATGGACTGGAGCTCATCTGCAAAAGGCCCTCTTGTAAGACTGGTTTT
-----+-----+-----+-----+-----+
1321 CTGCCAATGACCACCAAGCCCAAGATTTTCCTCTTGTGATTTCTTTAAAGAATGACTATA
-----+-----+-----+-----+-----+
1381 TAAATTTATTCCTACTAAAAATATTGTTTCTGCAATTCATTTTATAGCAACAACAATTGGT
-----+-----+-----+-----+-----+
1441 AAACTCACTGTGATCAATAATTTTATATCATGCACAAATATGTTTAAATAAATGAAAA
-----+-----+-----+-----+-----+
1501 TTGTATTATAAAAAA
-----+-----+-----+-----+-----+

FIG. 2D

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1 50
Pd gfa .MRTLACLLL LCGYLAVHL AEEAEIPREV IERLARSQIH SIRDQLRLE
Pd gfb MNRCWA.LFL SLCCYLRLVS AEGDPIPEEL YEMLSOHSIR SFDDLQRLH
VegfMNFL SWHWSLALL LY.....LHAKWSQA
Vegf2MTV LYPEYKMYK CQ.....LRKGGWQH

51 100
Pd gfa IDSVGSEDSL DTSRAHGVH ATKHVPEKRP LPIRRKRSI.EEAVP
Pd gfb GDP.GEEDGA ELDLNMTRSH SGGELES... .LARGRRSLG SLTIAEPAMI
Vegf APMAE.....GGGQ NHHEVVKFMD .VYQR.....
Vegf2 REQANLNSRT EETIKFAAAH YNTEILKSID NEWRK.....

101 150
Pd gfa AVCKTRTVIY EIPRSQVDPT SANFLIWPCC VEKRCCTGCC NTSSVKQPS
Pd gfb AECKTRTEVF EISRRLDRT NANFLVWPPC VEVQRCSCCC NNRNVQCRPT
Vegf SYCHPIETLV DIFOEYPDEI ..EYIFKPSC VPLMRGCGCC NDEGLECVPT
Vegf2 TQCMPREVCI DVGKEFGVAT ..NTFFKPPC VSVYRCGGCC NSEGLQCMNT

151 200
Pd gfa RVHRSVKVA KVEYVRKKPK LKEVQVRLEE HLEQAC.....AT.....
Pd gfb QVQLRPVQVR KIEIVRKKPI FKKATVTLED HLAQKQ.....ETVAAARPVT
Vegf EESNITMQIM RIK.PH..QG QHIGEMSFLQ HNKCECRPKK DRARQEKKS
Vegf2 STSYLSKTLF EIT.VPLSQG PKPVTISFAN HTSCRCMSKL DVYRQVHSII

FIG. 3A



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201
Pd gfa TSLNPD YREEDTDVR. 250
Pd gfb RSPGCSQEQ AKTPQIRVTI RTVRVRPPK GKHKFKHITH DKTALKETLG
Veg f RGK..... .GKGQKRKRK KSRYKSWSVY VGARCCCLMPW SLPGPHP
Veg f2 RRSPLATLPQ CQAANKTCPT NYMNNHICR CLAQEDFMFS SDAGDDSTDG

251
Pd gfa 300
Pd gfb A.....
Veg f CGP CSE RRKHLFVQDP QTCKCCKNT
Veg f2 FHDICGNKE LDEETCQCVC RAGLRPASC G PHKEL...DR NSCQCVCCKNK

301
Pd gfa 350
Pd gfb
Veg f ..DSRCKARQ LELNERTC RC DKPRR.....
Veg f2 LFPSQCGANR .EFDENTCQC VCKRTCPRNQ PLNPGKCACE CTESPOKCLL

351
Pd gfa 398
Pd gfb
Veg f
Veg f2 KGKFFHHQTC SCYRRPCTNR QKACEPGFSY SEEVCRCVPS YWQRPQMS

FIG. 3B

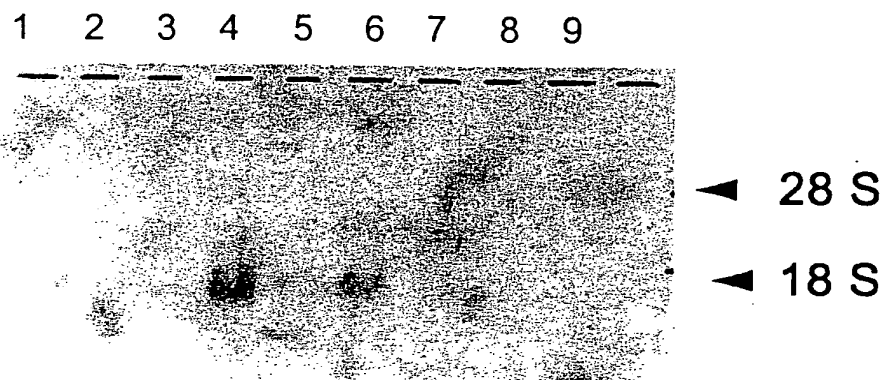


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PERCENTAGE (%) OF AMINO ACID IDENTITIES BETWEEN EACH PAIR OF GENES IS SHOWN IN THE FOLLOWING TABLE				
	PDGF α	PDGF β	VEGF	VEGF2
PDGF α				
PDGF β	48.0			
VEGF	20.7	22.7		
VEGF2	23.5	22.4	30.0	

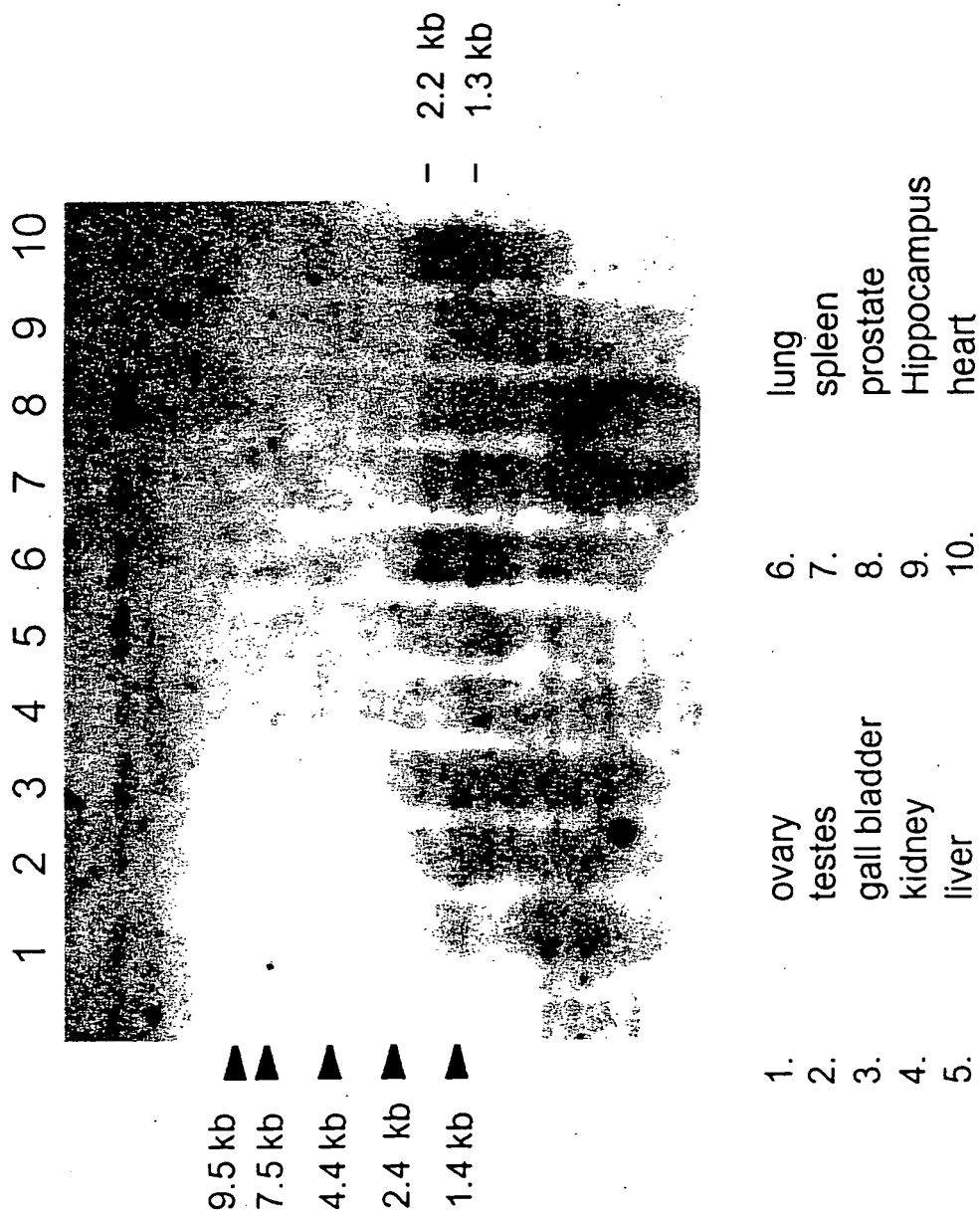
FIG.4

Expression of VEGF2 mRNA in
Human Breast Tumor Cells



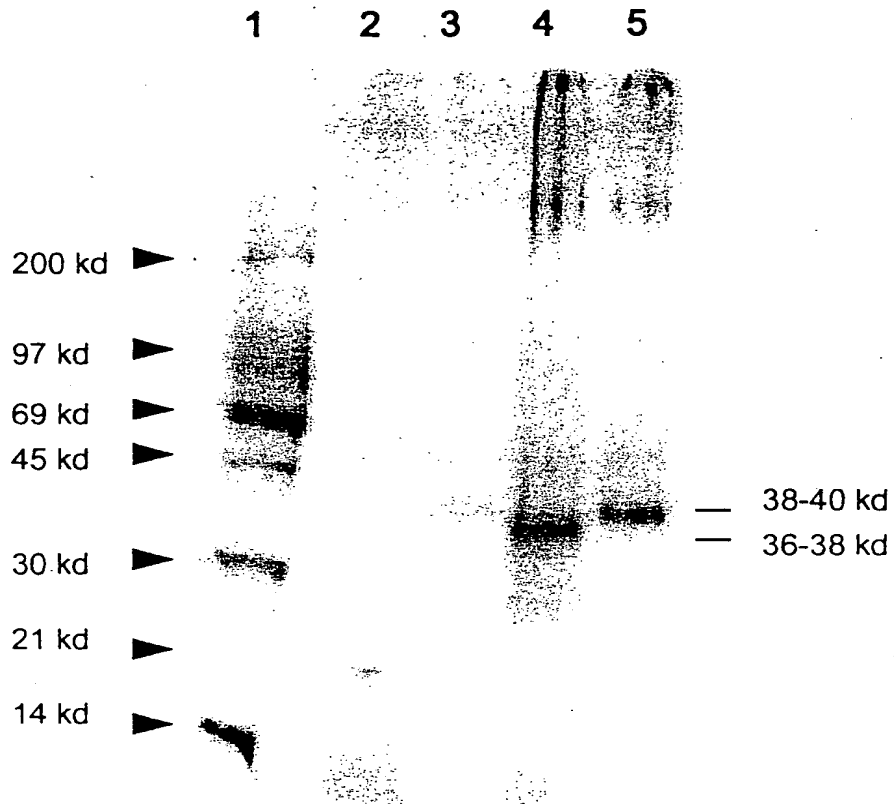
Lane 1. normal breast tissue
Lane 2. breast tumor tissue
Lane 3-9. breast tumor cell lines.

FIG.5



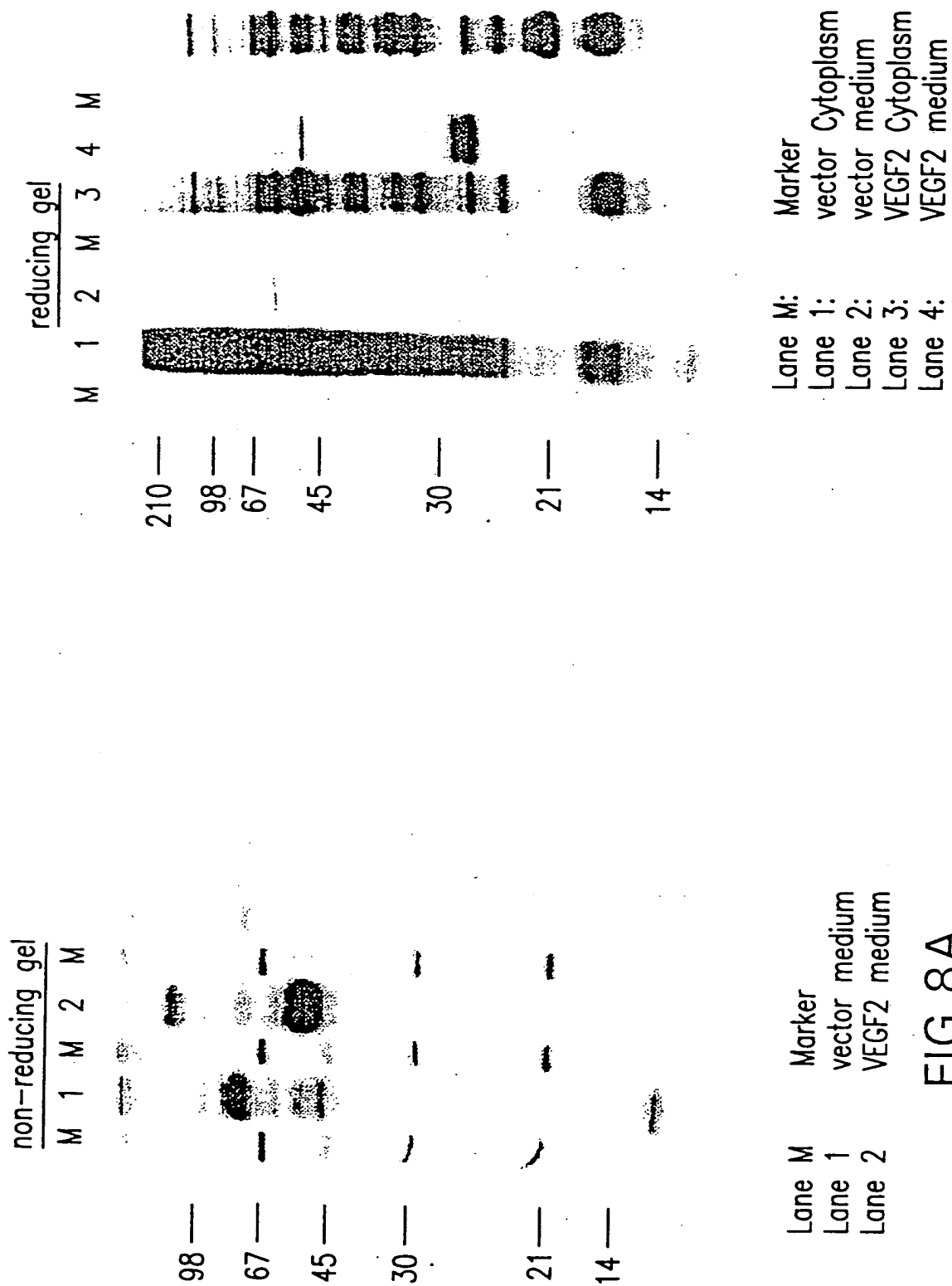
Expression of VEGF2 mRNA in human adult tissues.

FIG.6



Lane 1: 14-C and rainbow M.W. marker
Lane 2: FGF control
Lane 3: VEGF2 (M13-reverse & forward primers)
Lane 4: VEGF2 (M13-reverse & VEGF-F4 primers)
Lane 5: VEGF2 (M13-reverse & VEGF-F5 primers)

FIG.7



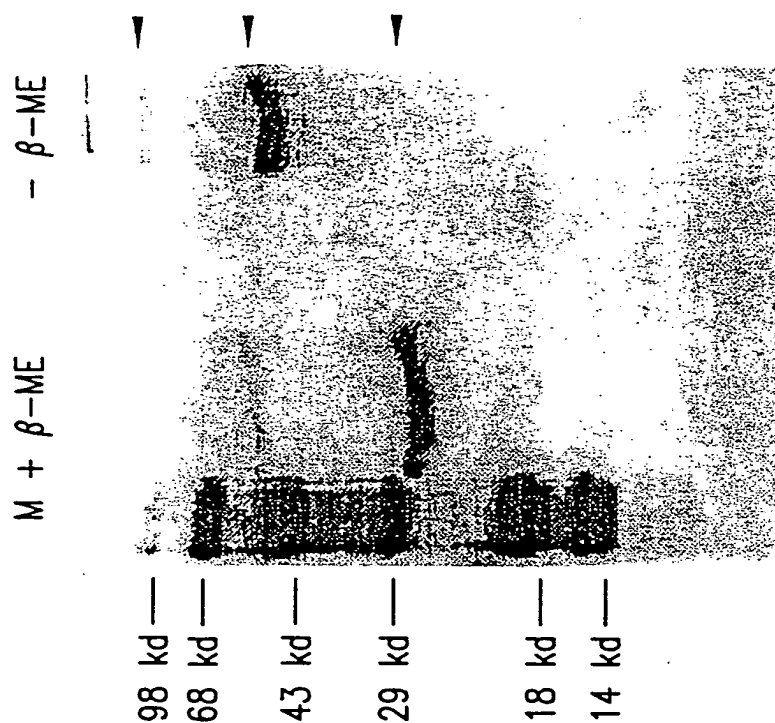
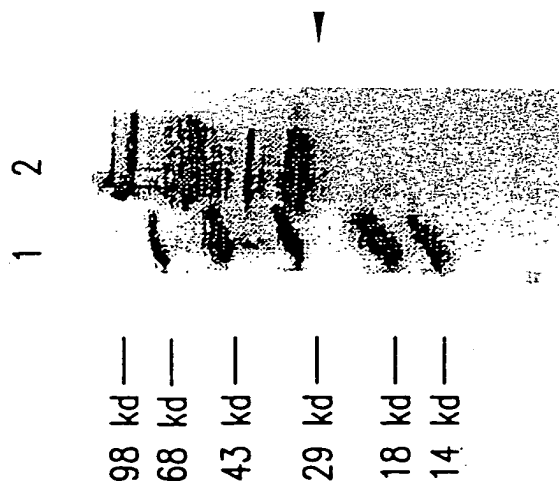


FIG.10



Lane 1: Molecular weight marker
 Lane 2: Precipitates containing VEGF2.

FIG.9

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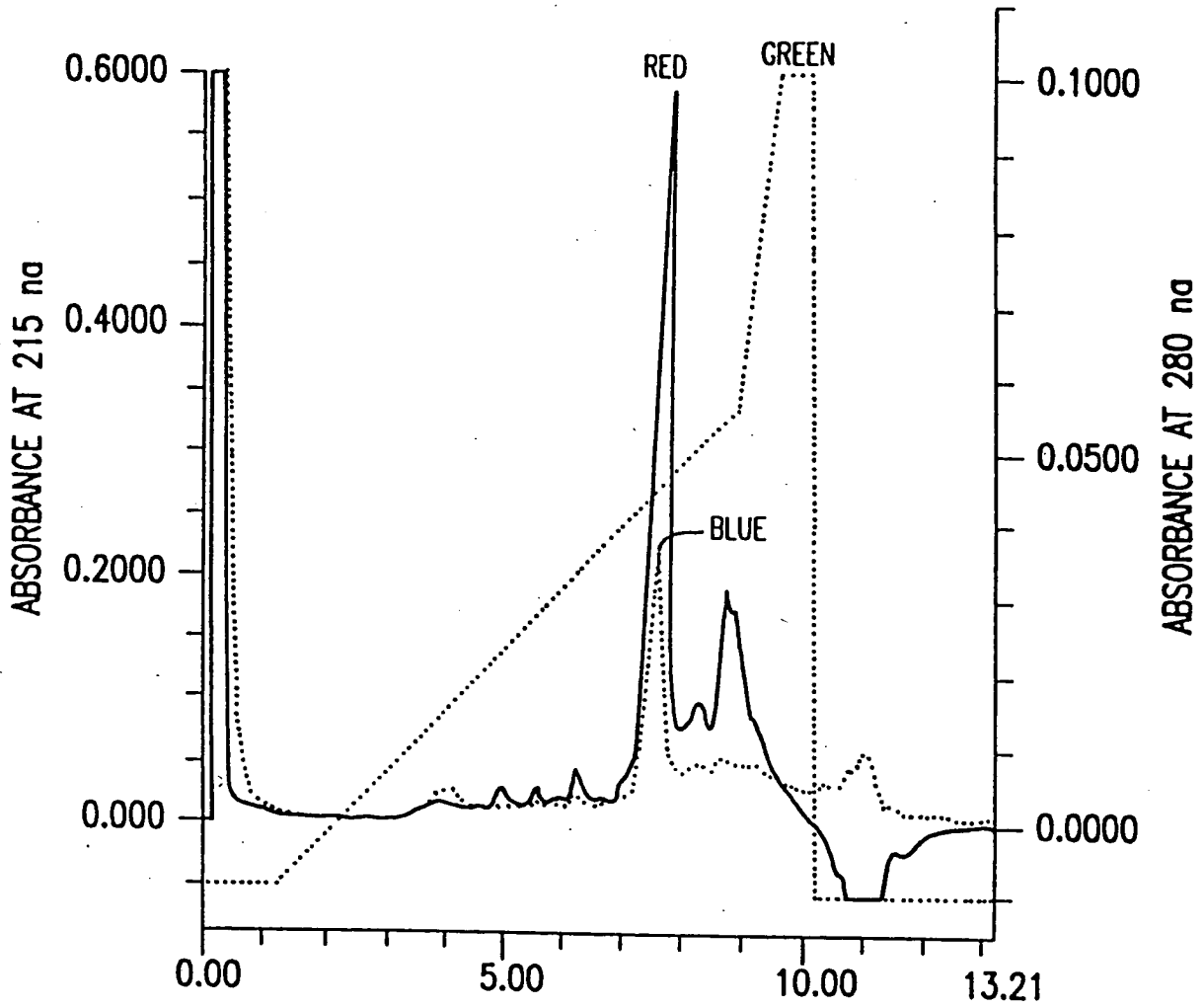


FIG. 11

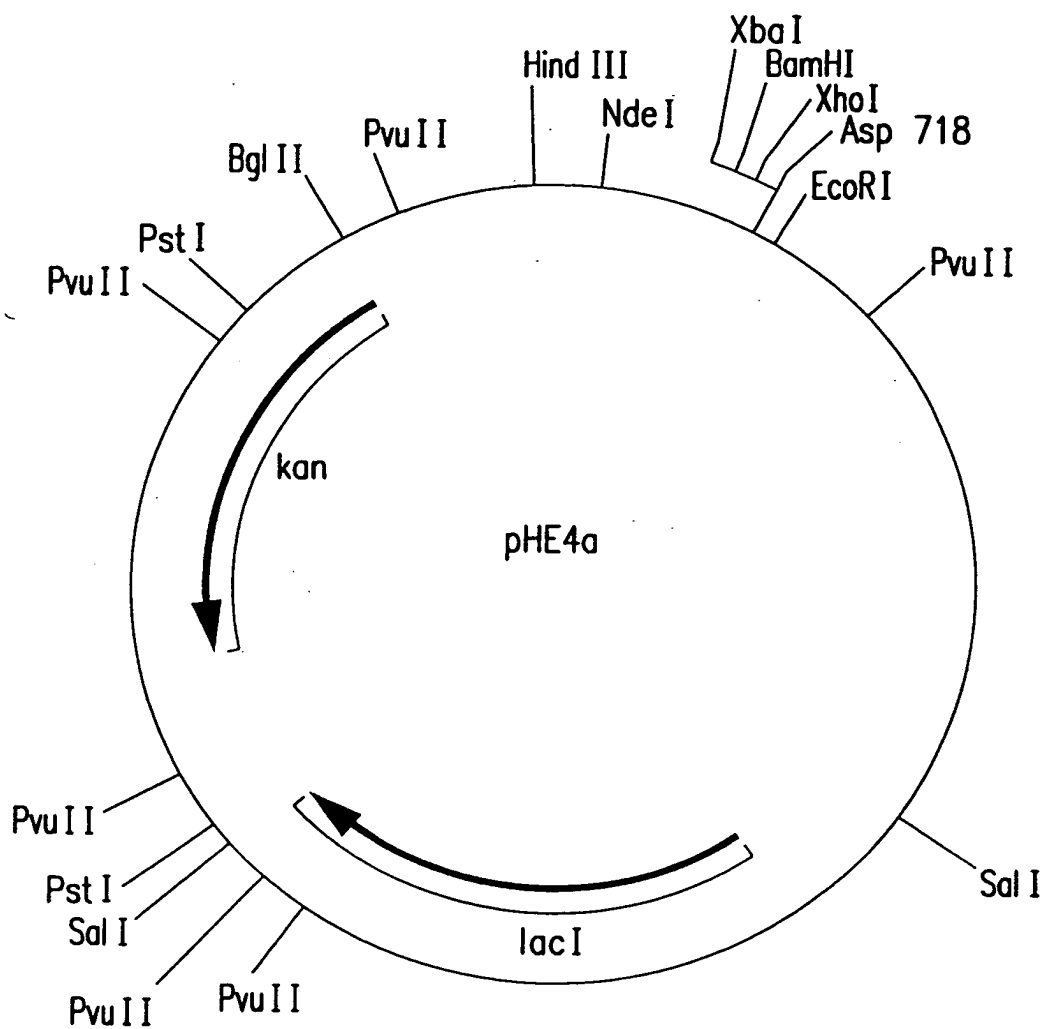


FIG.12



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-35 OPERATOR 1

1 AAGCTTAA AACTGCAAA AATAGT TTGACT(TGTGAGCGGATAAGAAAT)

OPERATOR 2

-10

50 TAAGATGTACCC(AATTGTGAGCGGATAACAAT)TTCACACATTAA

S/D

94 AGACGAGAAATTA CATATG

FIG.13

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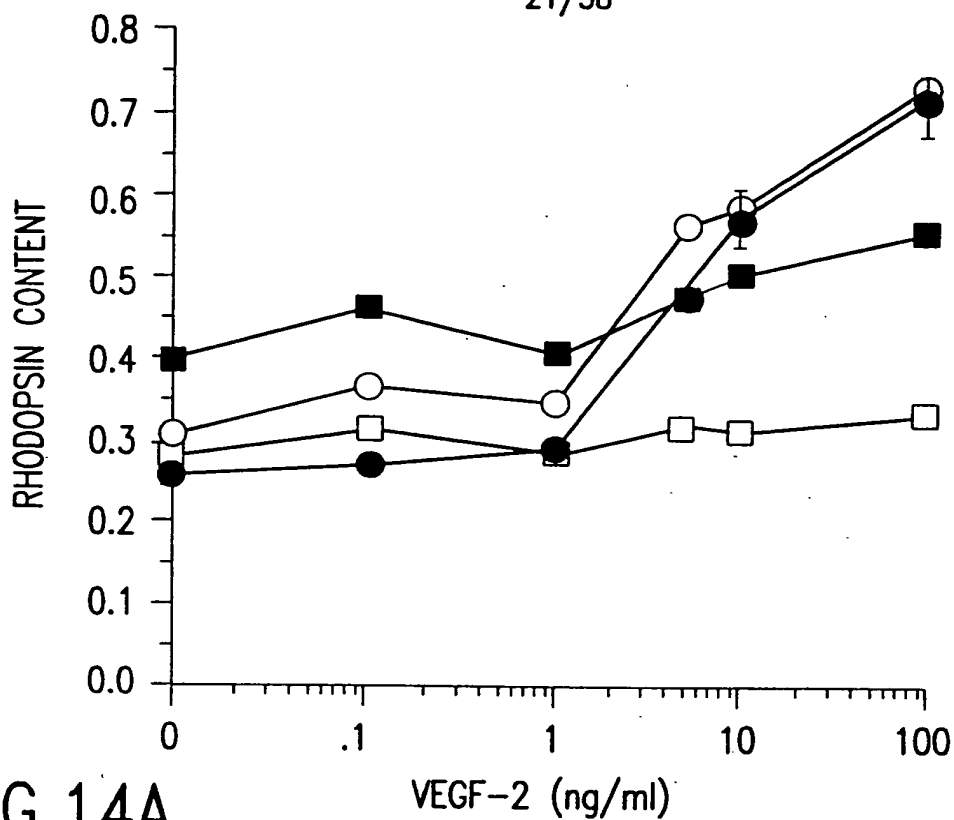


FIG.14A

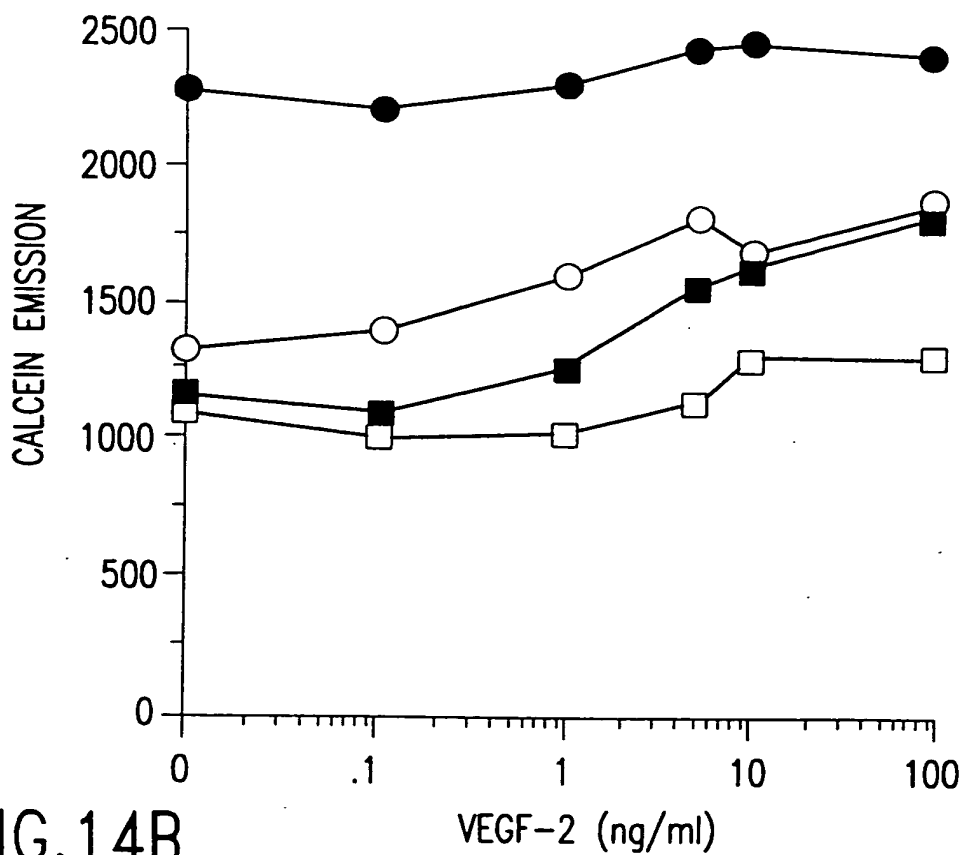


FIG.14B

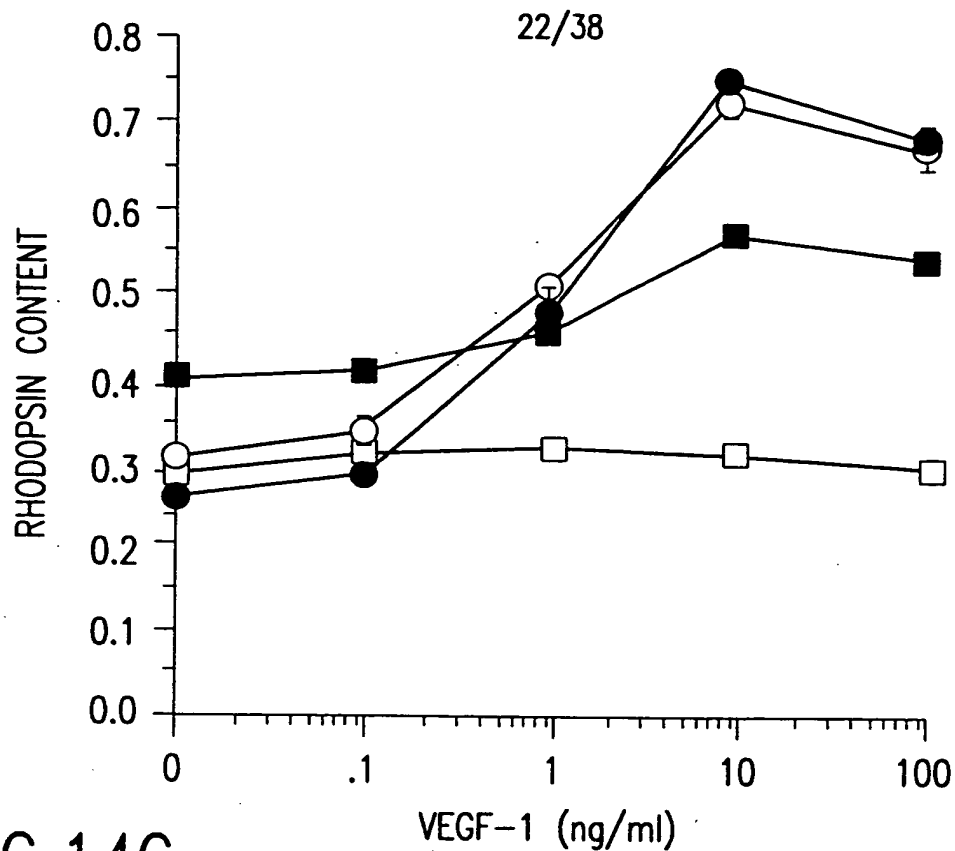


FIG.14C

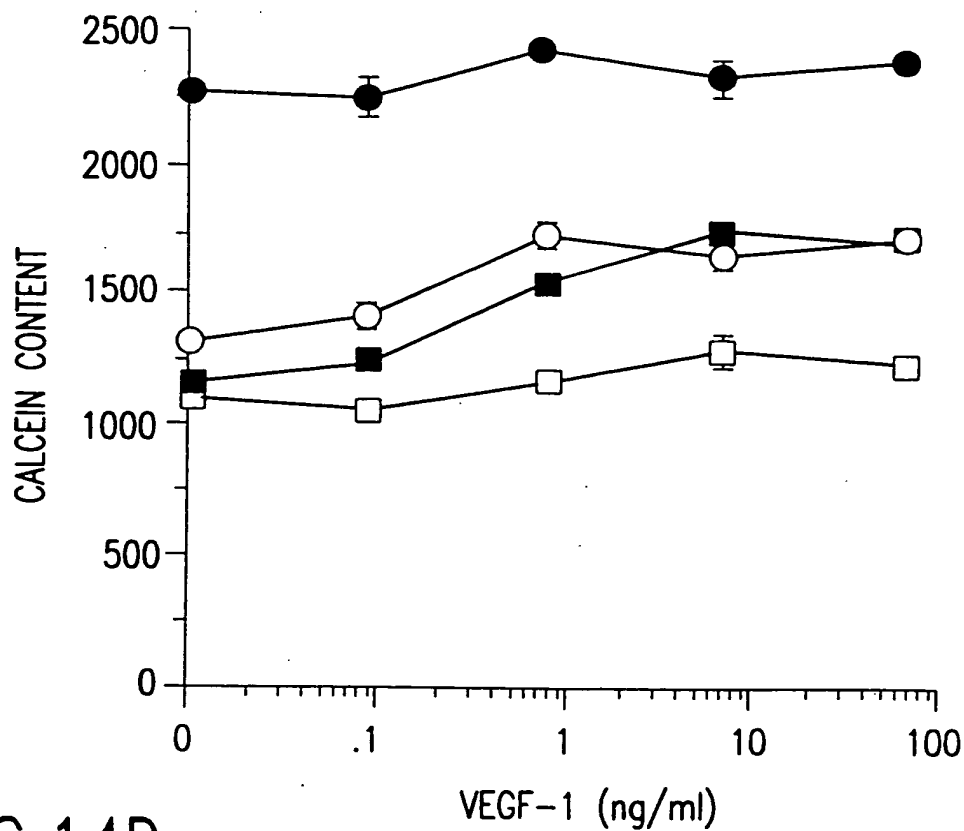


FIG.14D

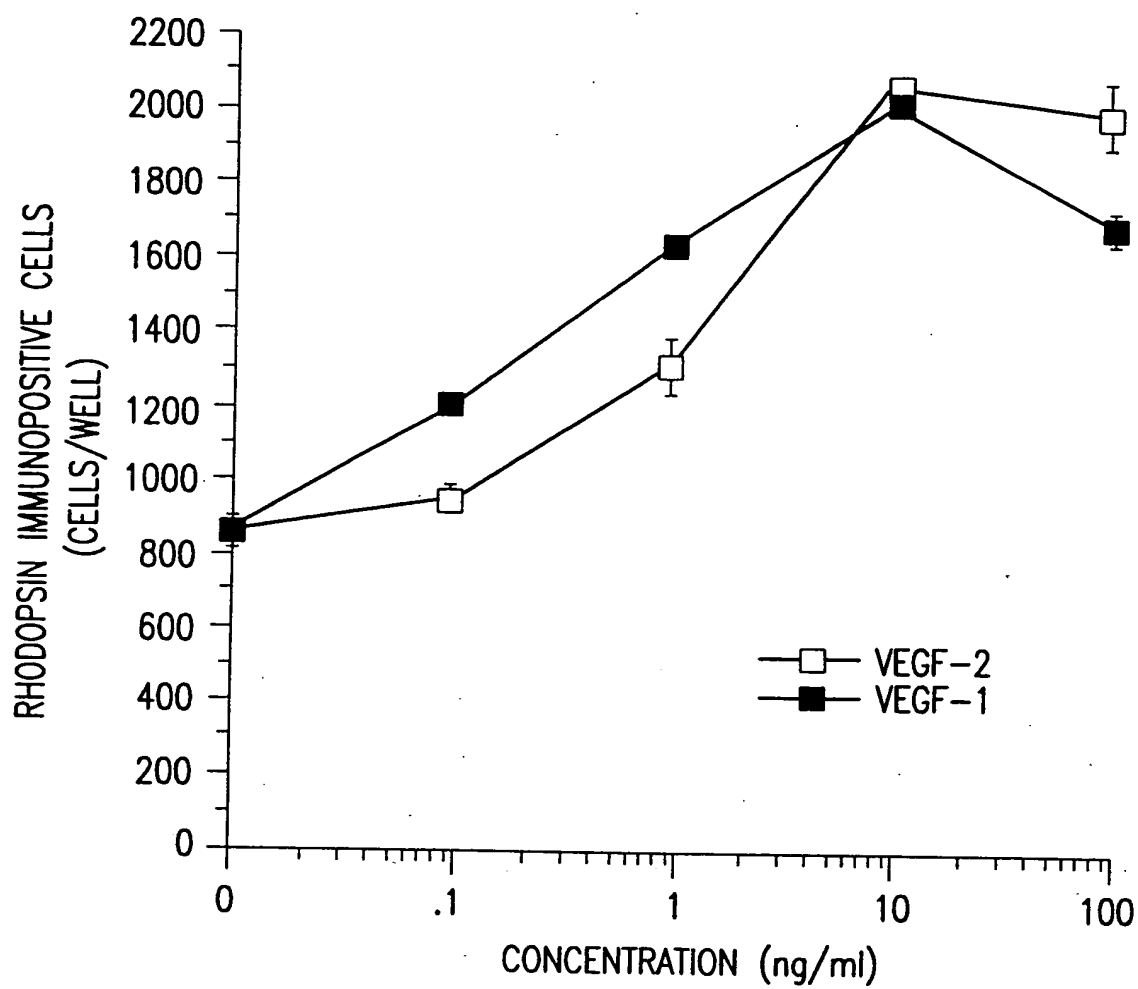


FIG.15

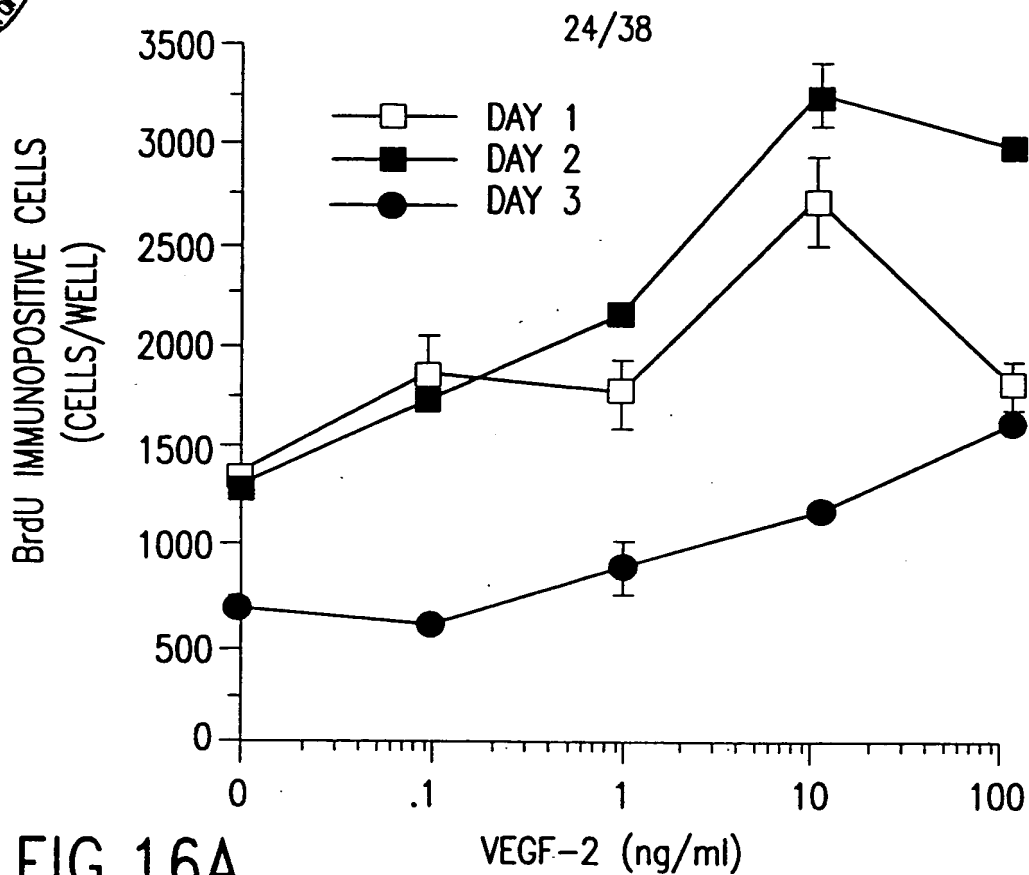


FIG.16A

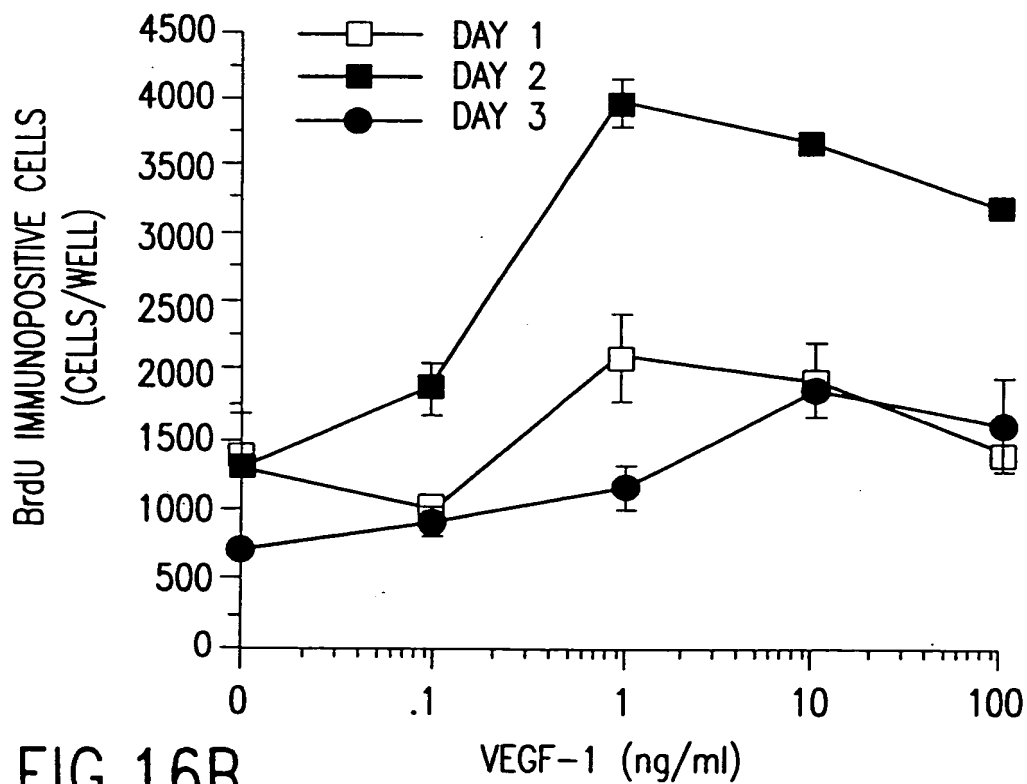


FIG.16B

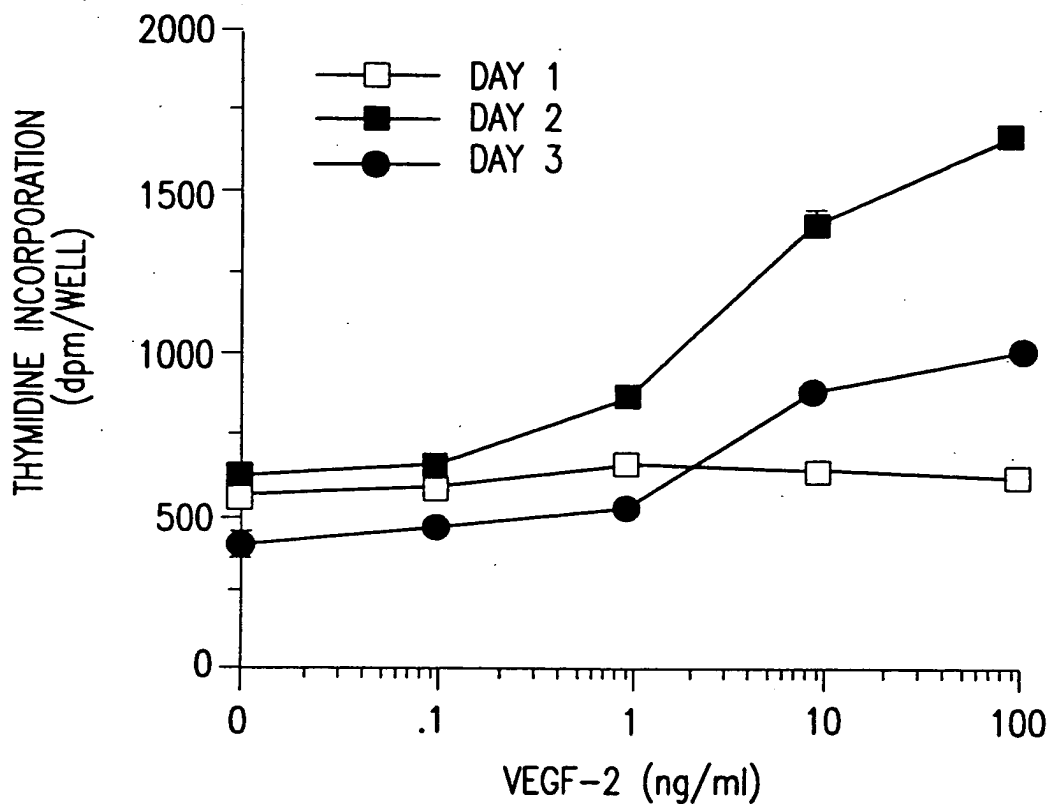


FIG.16C

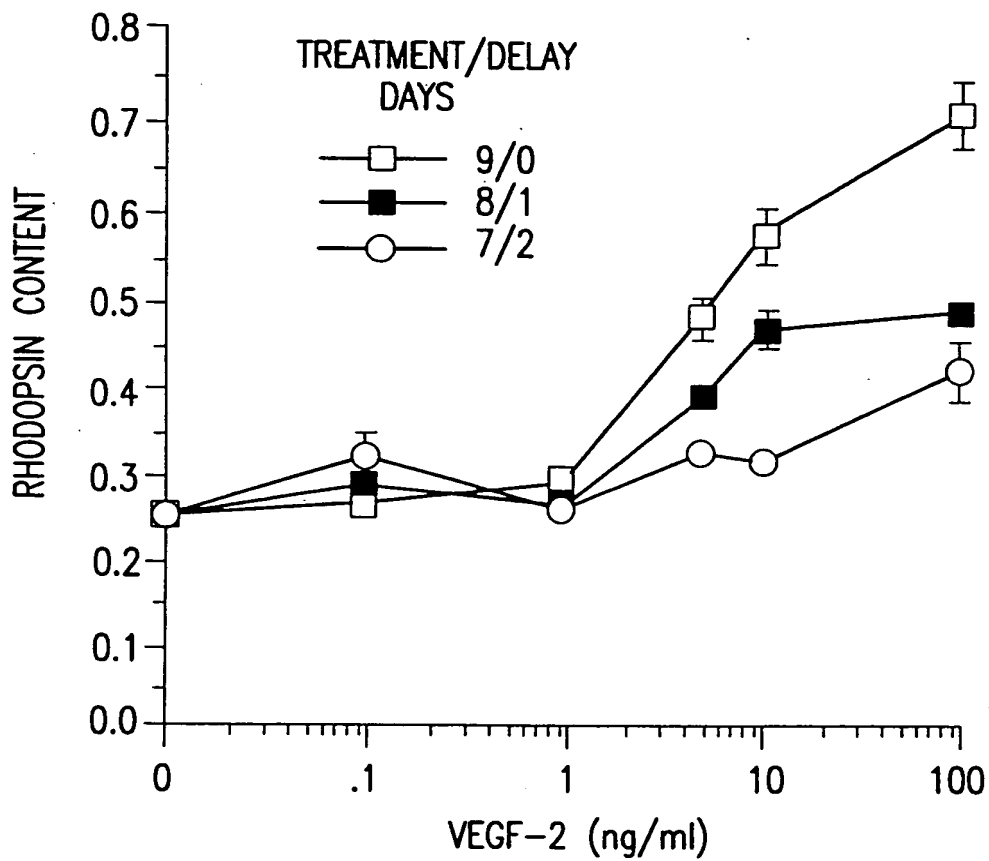


FIG.17A

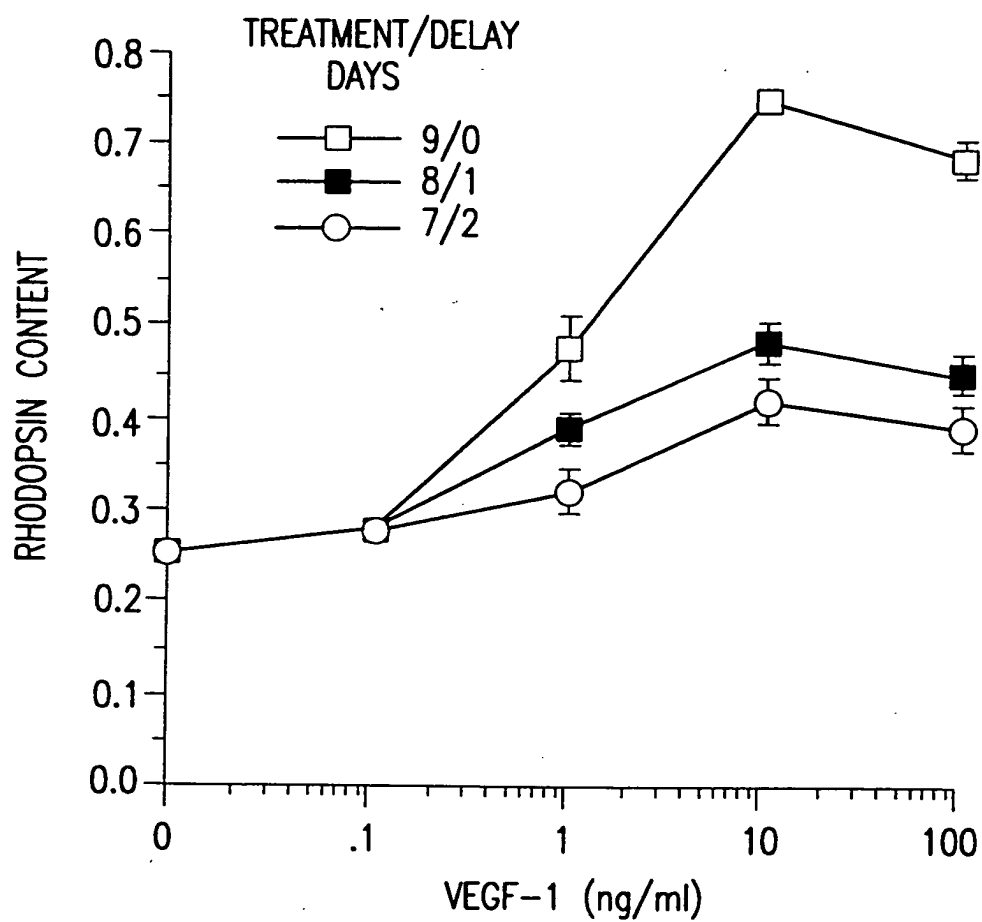


FIG.17B

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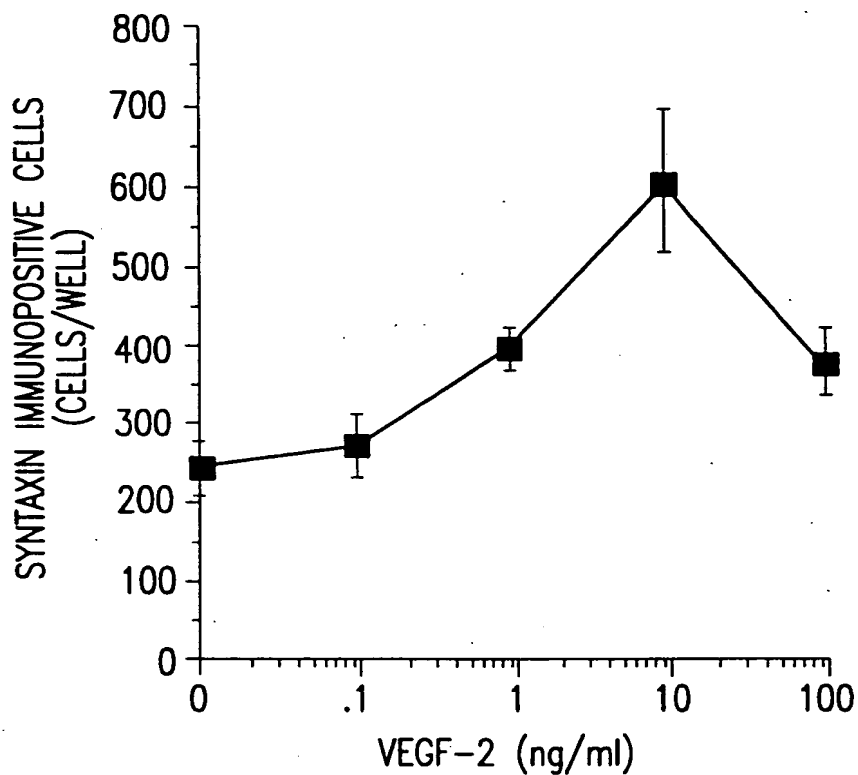


FIG.18A

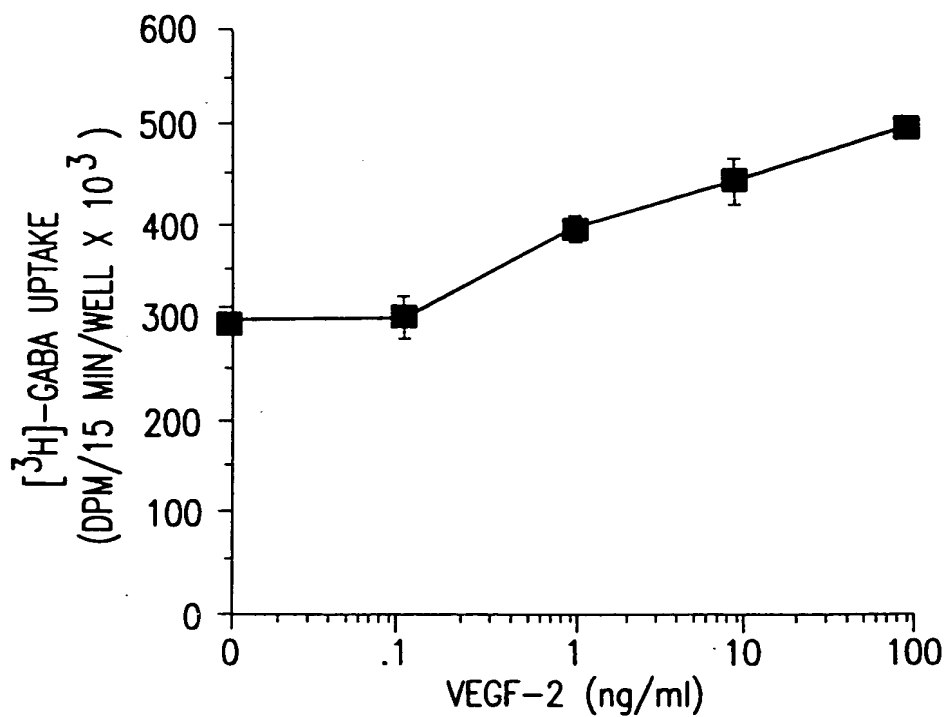


FIG.18B

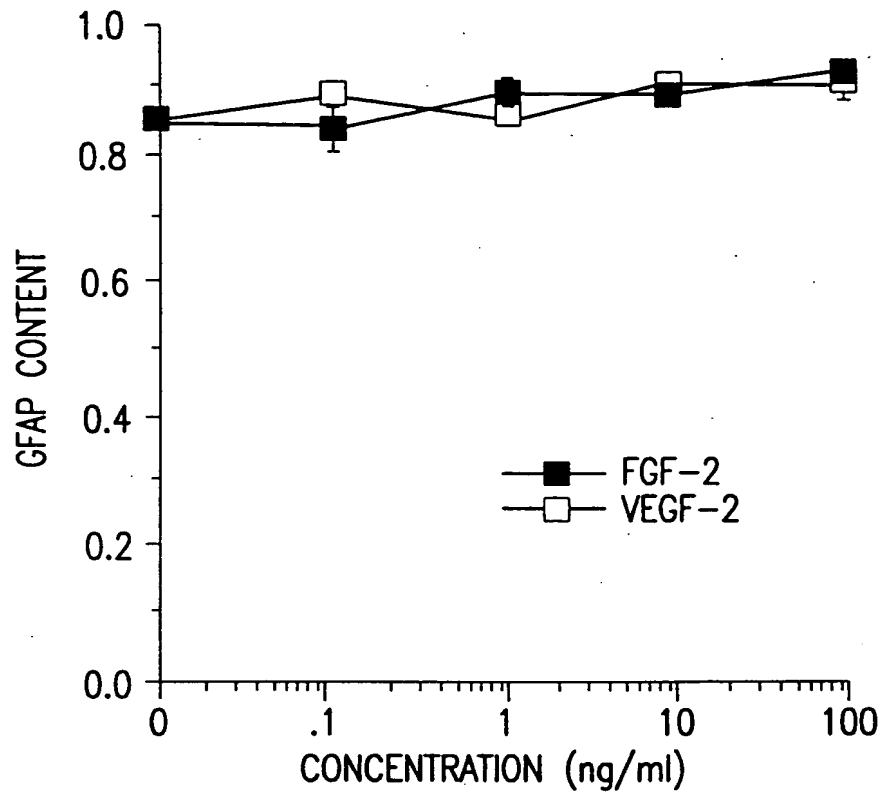


FIG.18C

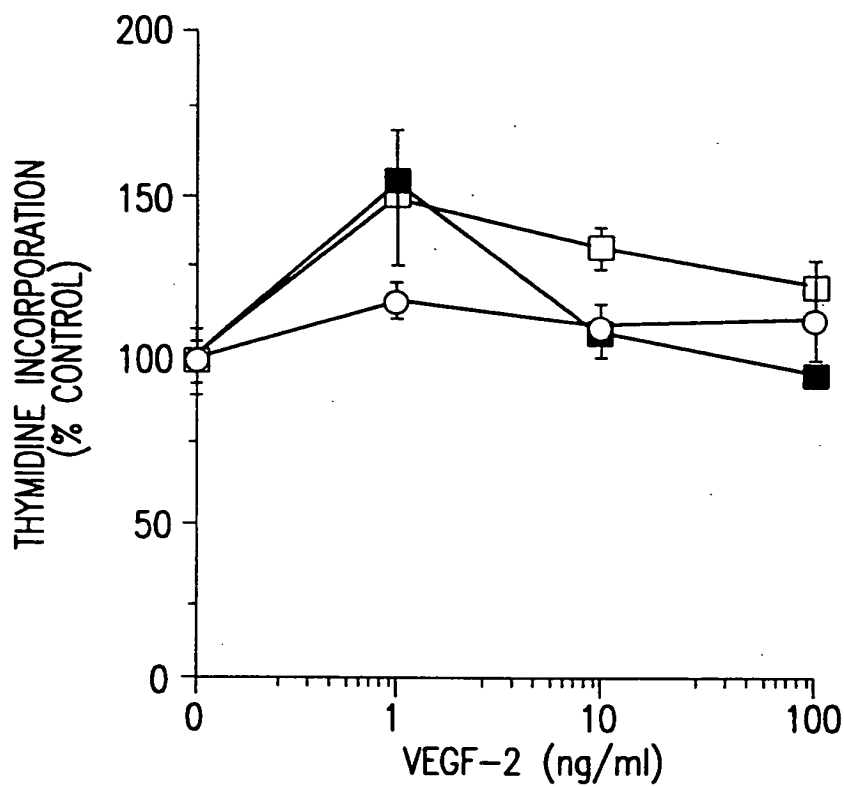


FIG.19A

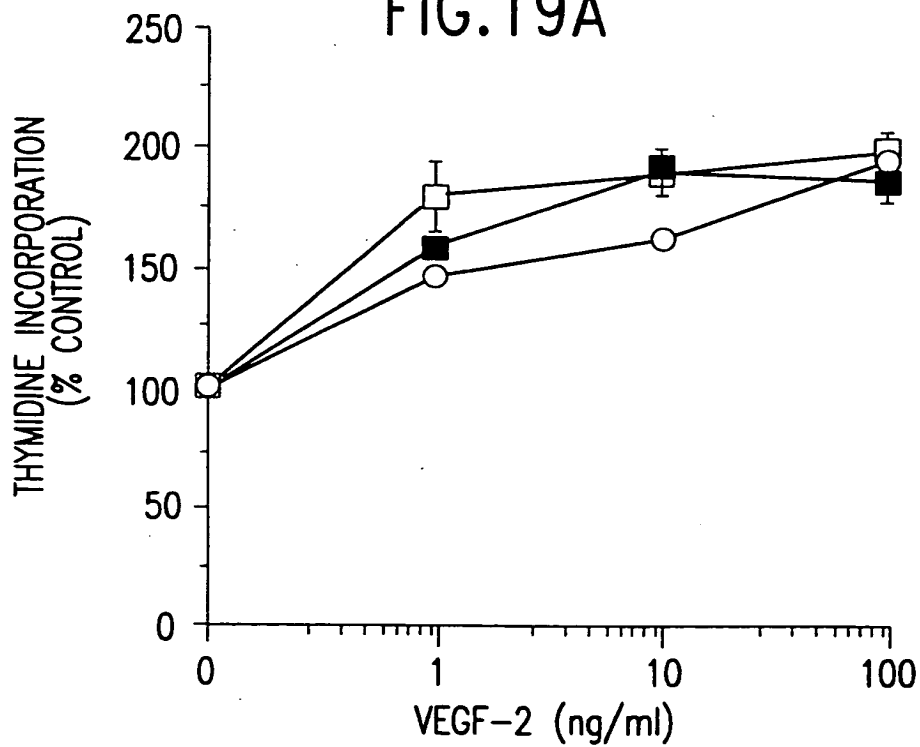


FIG.19B

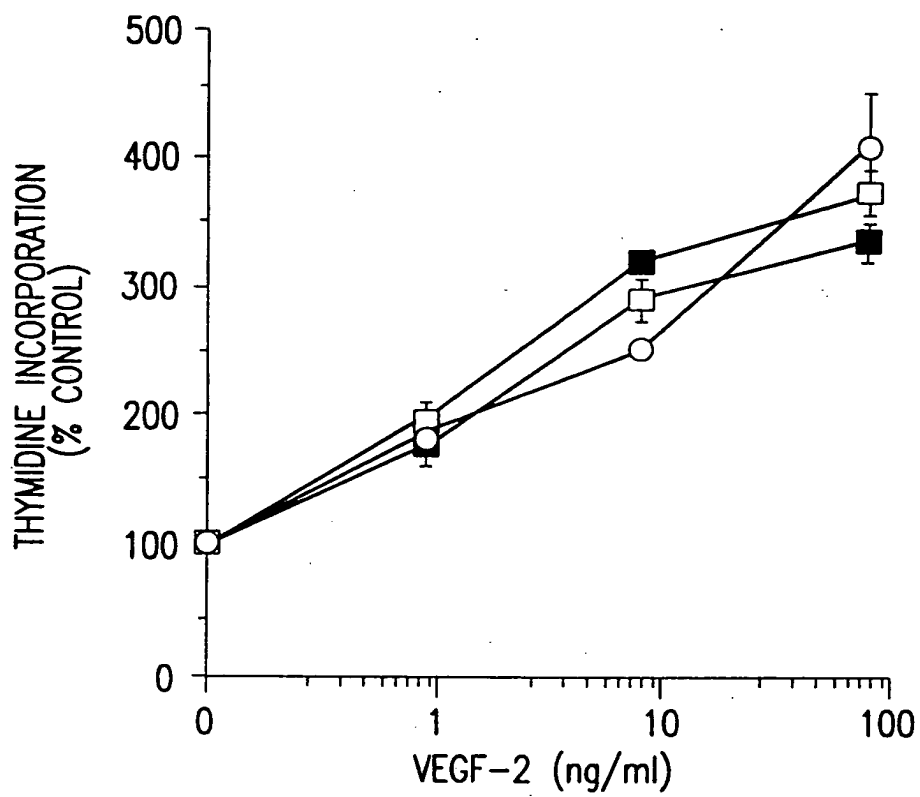


FIG.19C

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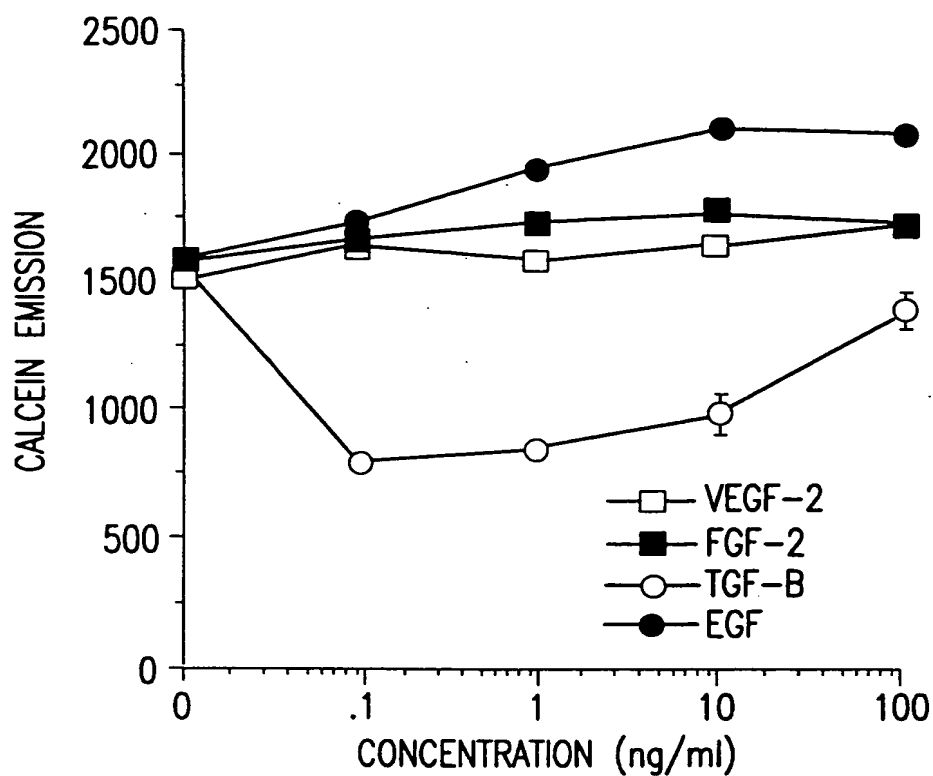


FIG.20A

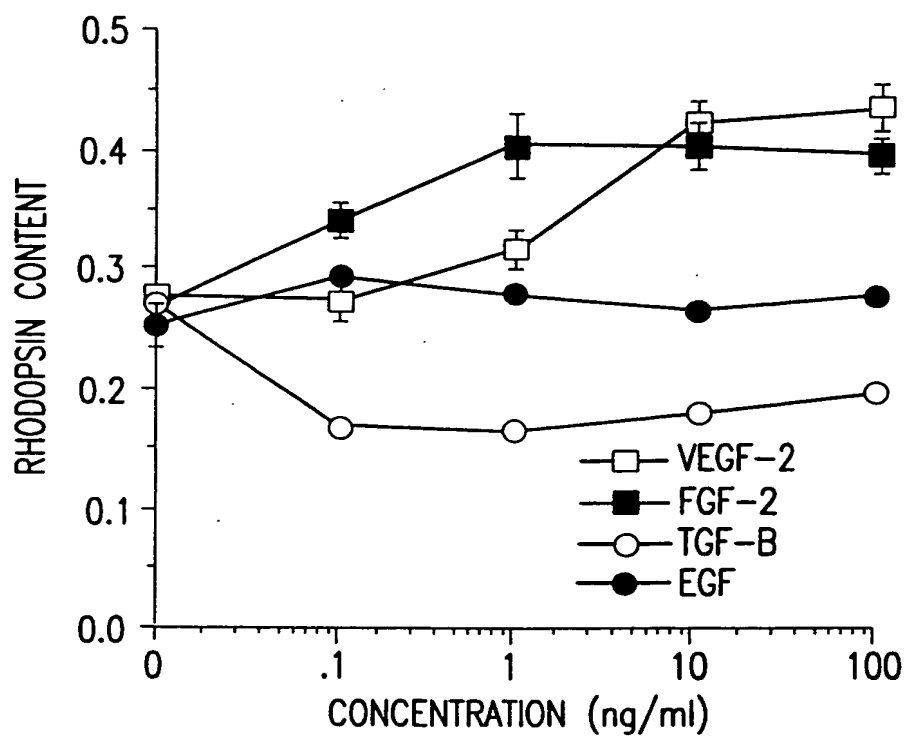


FIG.20B

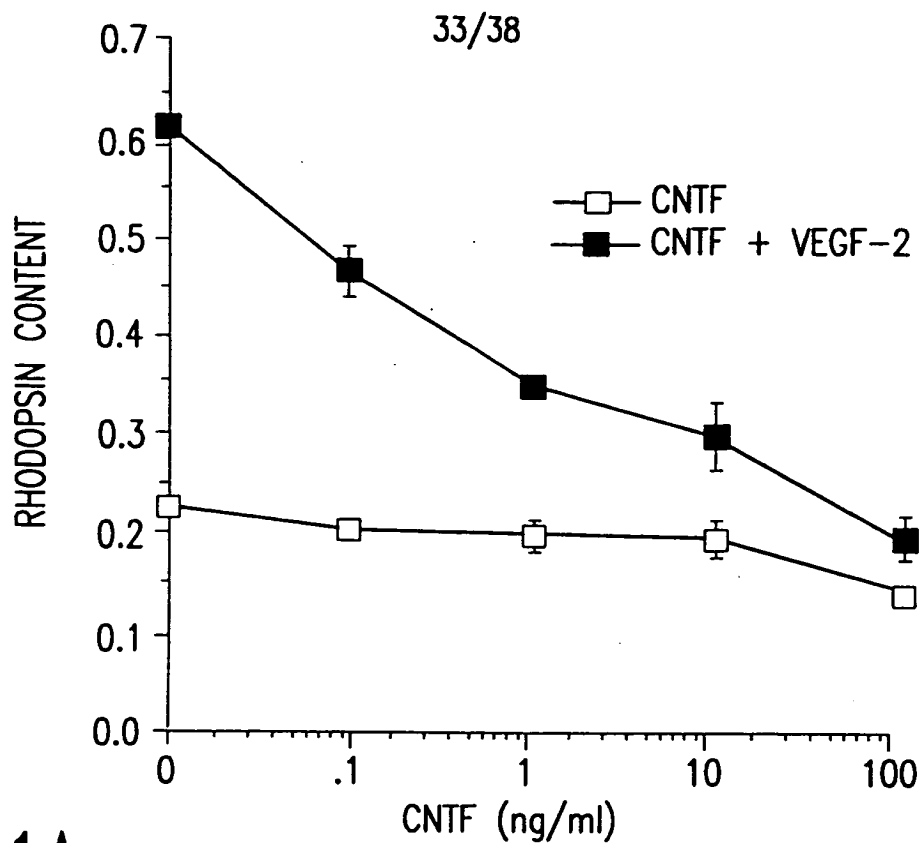


FIG.21A

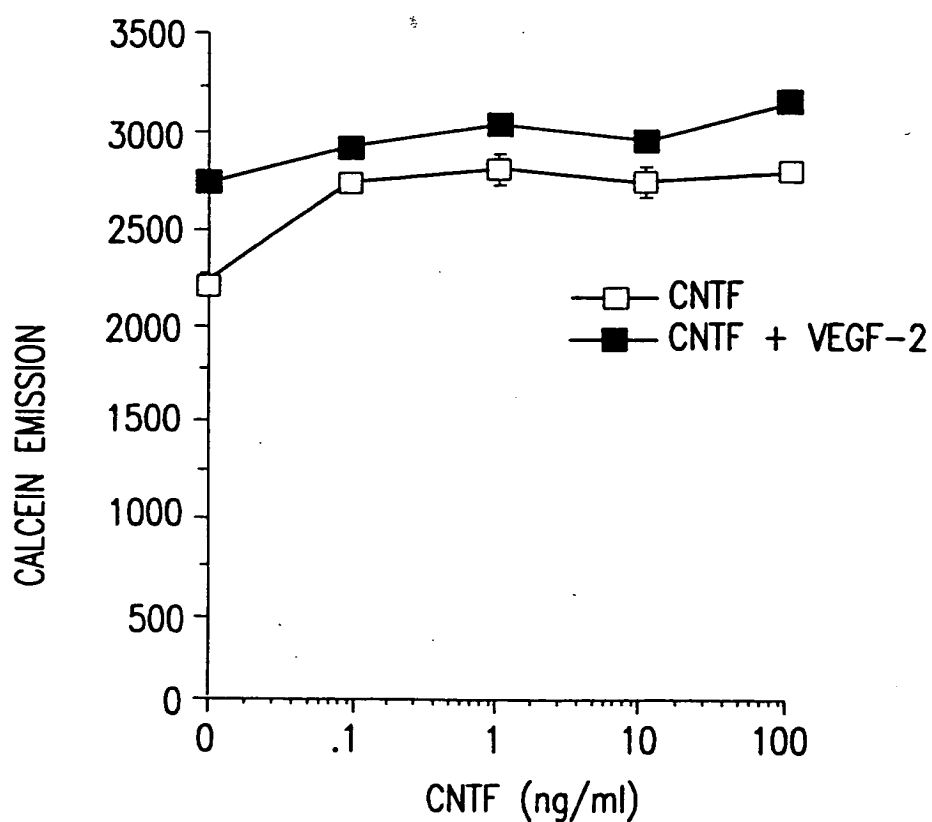


FIG.21B

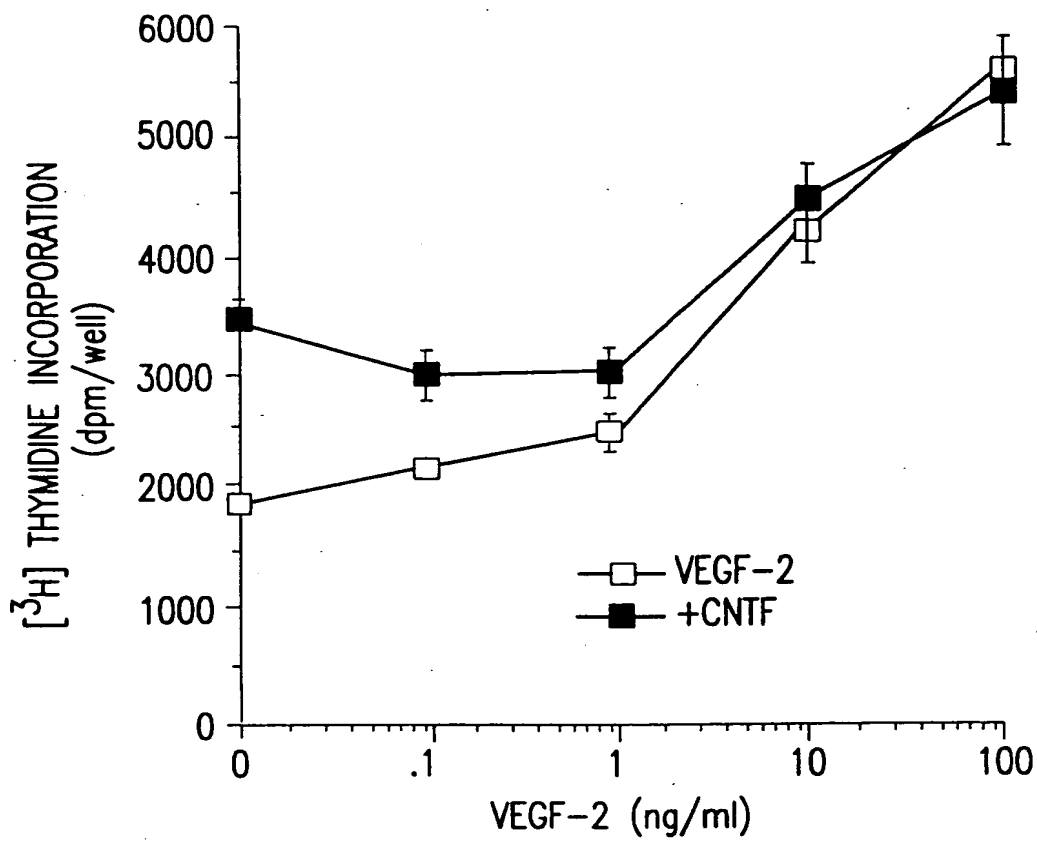


FIG.21C

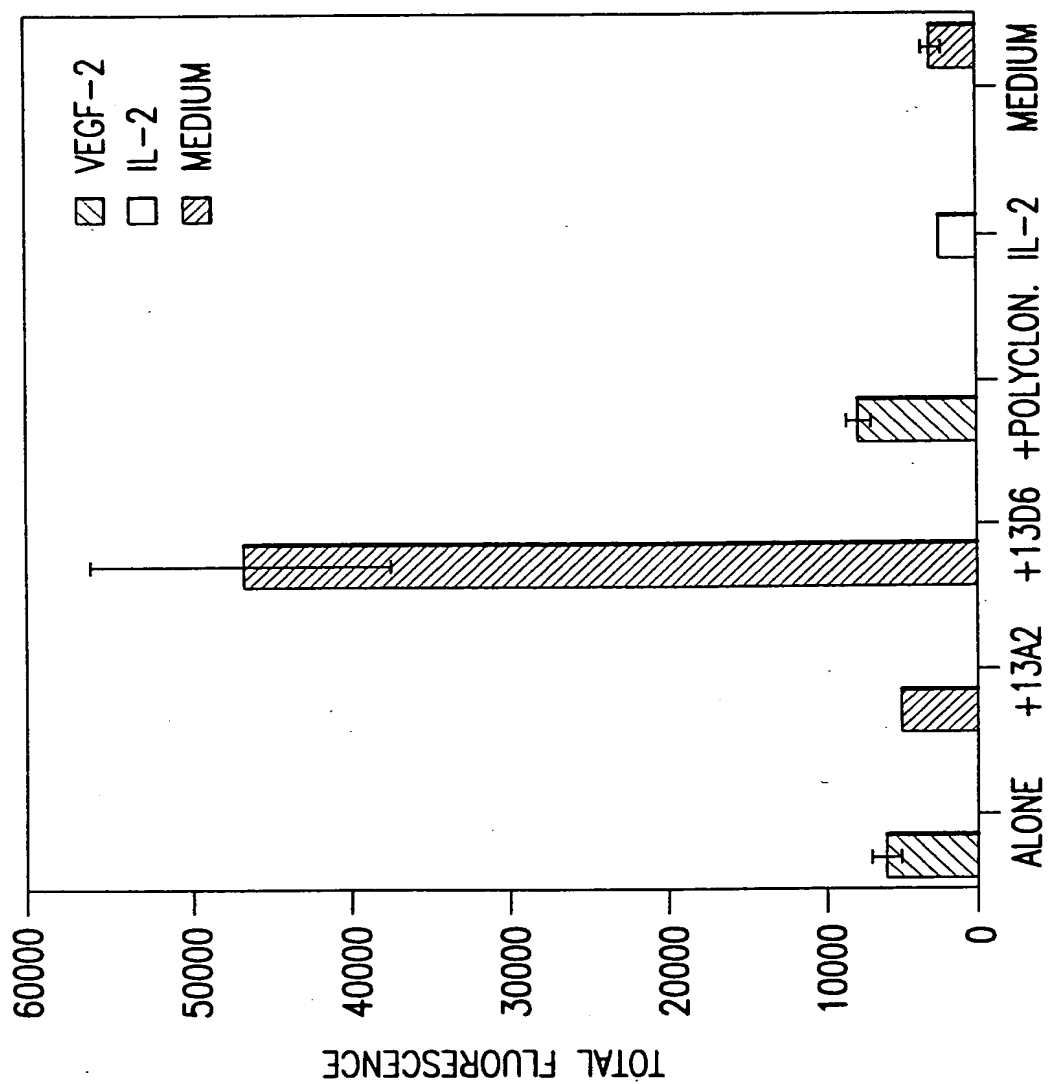


FIG. 22

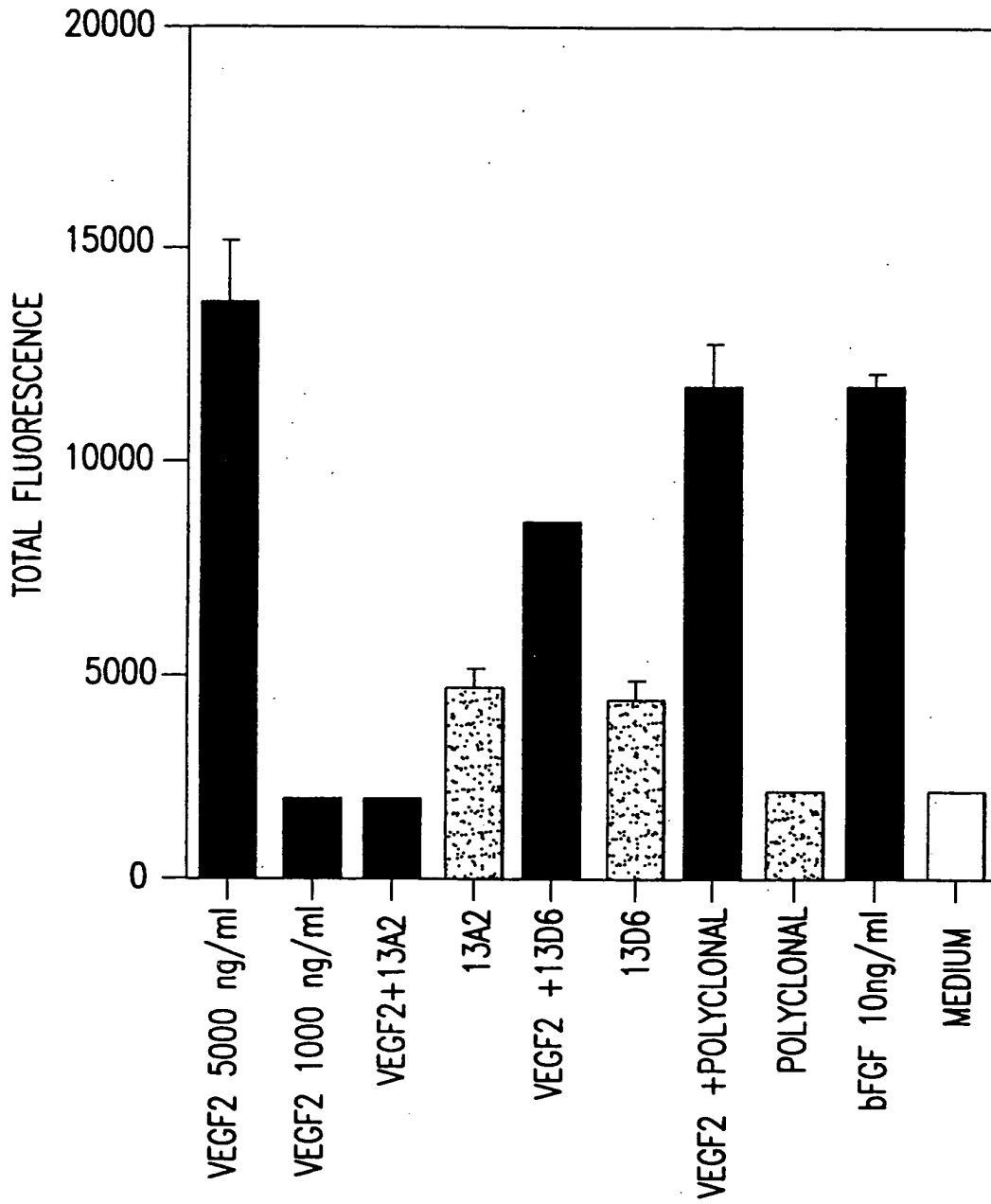


FIG.23

EPITOPE MAP FOR MURINE ANTI VEGF-2 MAB

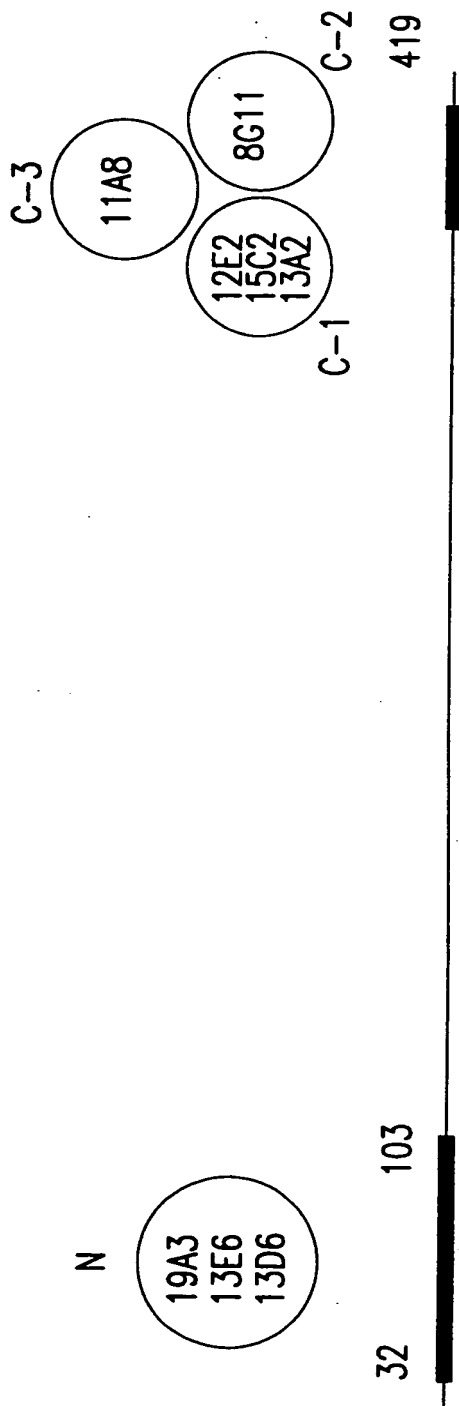


FIG.24



MURINE VEGF-2 MAB STATUS

	ISOTYPE	REL. AFFINITY ng/ml	SPECIFICITY	REACTIVITY		PURIFIED mg
				WESTERN	ELISA	
12E2	γ 1	<1	C-1	+	+	27
13A2	γ 1	<1	C-1	n.t	+	27
15C2	γ 1	<1	C-1	n.t	+	10
13D6	γ 1	<1	N	+	+	25
13E6	γ 1	1	N	+	+	38
19A3	γ 1	1	N	+	+	54
8G11	γ 1	5	C-2	+	+	7
11A8	γ 1	<1	C-3	+	+	9

FIG.25